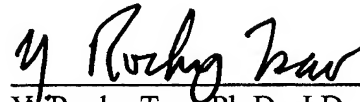## REMARKS

Applicants hereby submit that the enclosures fulfill the requirements under
37 CFR § 1.821-1.825. The amendments in the specification merely insert the paper copy of the
Sequence Listing and sequence identifiers in the specification. I hereby state that this
submission, filed in accordance with 37 CFR § 1.821(g), does not contain new matter.

Please apply any charges to deposit account 06-1050, referencing attorney-docket 12669-002001.

Respectfully submitted,

Date: 3-1-05

Rocky Tsao Ph.D., J.D
Reg. No. 34,053

PTO Customer No. 26161
Fish & Richardson P.C.
225 Franklin Street
Boston, MA 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

21034640.doc

	Application No.	Applicant(s)	
Notice to Comply	**Examiner** G.R.Ewoldt, Ph.D.	**Art Unit** 1644	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: see enclosed communication

Applicant Must Provide:
☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216 or (703) 308-2923
For CRF Submission Help, call (703) 308-4212 or 308-2923
PatentIn Software Program Support
    Technical Assistance.......................................703-287-0200
    To Purchase PatentIn Software.......................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : John David Fraser et al   Art Unit : 1644
Serial No. : 10/006,797   Examiner : Gerald R..Ewoldt
Filed : December 4, 2001
Title : IMMUNOMODULATORY CONSTRUCTS AND THEIR USES

MAIL STOP SEQUENCE
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

VERIFIED STATEMENT UNDER 37 CFR §1.821(f)

I, Katica Magovcevic, declare that I personally prepared the paper and the computer-readable copy of the Sequence Listing filed herewith for the above-identified application and that the content of both is the same.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of The United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: 2/24/2005

_____
Katica Magovcevic

Fish & Richardson P.C.
225 Franklin Street
Boston, MA 02110-2804
(617) 542-5070 telephone
(617) 542-8906 facsimile

21033651.doc

SEQUENCE LISTING

<110> Fraser, John David
       Nicholson, Melissa Joy

<120> Immunomodulatory Constructs And Their
       Uses

<130> 12669-002001

<140> US 10/006,797
<141> 2001-12-04

<150> US 60/251,243
<151> 2000-12-04

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 621
<212> DNA
<213> Streptococcus pyogenes

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actcaaaaat atagagggaa agactattat attagttccg aaatgtctta tgaggcctct 180
caaaaattta aacgagatga tcatgtagat gttttggat tattttatat tcttaattct 240
cacaccggtg agtacatcta tggaggaatt acgcctgctc aaaataataa agtaaatcat 300
aaattattgg gaaatctatt tatttcggga gaatctcaac agaacttaaa taacaagatt 360
attctagaaa aggatatcgt aactttccag gaaattgact ttaaaatcag aaaatacctt 420
atggataatt ataaaattta tgacgctact tctccttatg taagcggcag aatcgaaatt 480
ggcacaaaag atgggaaaca tgagcaaata gacttatttg actcaccaaa tgaagggact 540
agatcagata tttttgcaaa atataaagat aatagaatta tcaatatgaa gaactttagt 600
catttcgata tttatcttga a                                           621
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<210> 2
<211> 207
<212> PRT
<213> Streptococcus pyogenes

<400> 2
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Asp Ser Lys Lys Asp Ile Ser Asn Val Lys Ser Asp Leu Leu Tyr Ala
 1               5                  10                  15
Tyr Thr Ile Thr Pro Tyr Asp Tyr Lys Asp Cys Arg Val Asn Phe Ser
            20                  25                  30
Thr Thr His Thr Leu Asn Ile Asp Thr Gln Lys Tyr Arg Gly Lys Asp
        35                  40                  45
Tyr Tyr Ile Ser Ser Glu Met Ser Tyr Glu Ala Ser Gln Lys Phe Lys
    50                  55                  60
Arg Asp Asp His Val Asp Val Phe Gly Leu Phe Tyr Ile Leu Asn Ser
65                  70                  75                  80
His Thr Gly Glu Tyr Ile Tyr Gly Gly Ile Thr Pro Ala Gln Asn Asn
```

```
                    85                    90                    95
Lys Val Asn His Lys Leu Leu Gly Asn Leu Phe Ile Ser Gly Glu Ser
                    100                   105                   110
Gln Gln Asn Leu Asn Asn Lys Ile Ile Leu Glu Lys Asp Ile Val Thr
            115                   120                   125
Phe Gln Glu Ile Asp Phe Lys Ile Arg Lys Tyr Leu Met Asp Asn Tyr
        130                   135                   140
Lys Ile Tyr Asp Ala Thr Ser Pro Tyr Val Ser Gly Arg Ile Glu Ile
145                   150                   155                   160
Gly Thr Lys Asp Gly Lys His Glu Gln Ile Asp Leu Phe Asp Ser Pro
                165                   170                   175
Asn Glu Gly Thr Arg Ser Asp Ile Phe Ala Lys Tyr Lys Asp Asn Arg
            180                   185                   190
Ile Ile Asn Met Lys Asn Phe Ser His Phe Asp Ile Tyr Leu Glu
        195                   200                   205
```

```
<210> 3
<211> 621
<212> DNA
<213> Artificial Sequence

<220>
<223> Combined mutants

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actcaaaaat atagagggaa agactattat attagttccg aaatgtctta tgaggcctct 180
caaaaattta acgagatga tcatgtagat gtttttggat tatttatat tctttgttct 240
cacaccggtg agtacatcta tggaggaatt acgcctgctc aaaataataa agtaaatcat 300
aaattattgg gaaatctatt tatttcggga gaatctcaac agaacttaaa taacaagatt 360
attctagaaa aggatatcgt aactttccag gaattgact ttaaaatcag aaaatacctt 420
atggataatt ataaaattta tgacgctact tctccttatg taagcggcag aatcgaaatt 480
ggcacaaaag atgggaaaca tgagcaaata gacttatttg actcaccaaa tgaagggact 540
caatcagata ttttttgcaaa atataaagat aatagaatta tcaatatgaa gaactttagt 600
catttcgata tttatcttga a                                          621
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<210> 4
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> Combined mutants

<400> 4
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 1               5                   10                  15
Tyr Thr Ile Thr Pro Tyr Asp Tyr Lys Asp Ser Arg Val Asn Phe Ser
            20                  25                  30
Thr Thr His Thr Leu Asn Ile Asp Thr Gln Lys Tyr Arg Gly Lys Asp
        35                  40                  45
Tyr Tyr Ile Ser Ser Glu Met Ser Tyr Glu Ala Ser Gln Lys Phe Lys
    50                  55                  60
Arg Asp Asp His Val Asp Val Phe Gly Leu Phe Tyr Ile Leu Cys Ser
65                  70                  75                  80
```

```
His Thr Gly Glu Tyr Ile Tyr Gly Gly Ile Thr Pro Ala Gln Asn Asn
                85                  90                  95
Lys Val Asn His Lys Leu Leu Gly Asn Leu Phe Ile Ser Gly Glu Ser
            100                 105                 110
Gln Gln Asn Leu Asn Asn Lys Ile Ile Leu Glu Lys Asp Ile Val Thr
            115                 120                 125
Phe Gln Glu Ile Asp Phe Lys Ile Arg Lys Tyr Leu Met Asp Asn Tyr
        130                 135                 140
Lys Ile Tyr Asp Ala Thr Ser Pro Tyr Val Ser Gly Arg Ile Glu Ile
145                 150                 155                 160
Gly Thr Lys Asp Gly Lys His Glu Gln Ile Asp Leu Phe Asp Ser Pro
                165                 170                 175
Asn Glu Gly Thr Gln Ser Asp Ile Phe Ala Lys Tyr Lys Asp Asn Arg
            180                 185                 190
Ile Ile Asn Met Lys Asn Phe Ser His Phe Asp Ile Tyr Leu Glu
            195                 200                 205
```

<210> 5
<211> 432
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> CDS
<222> (1)...(429)

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1               5                   10                  15

tac act ata act cct atc gaa ggt cgt acg cct gct caa aat aat aaa      96
Tyr Thr Ile Thr Pro Ile Glu Gly Arg Thr Pro Ala Gln Asn Asn Lys
            20                  25                  30

gta aat cat aaa tta ttg gga aat cta ttt att tcg gga gaa tct caa     144
Val Asn His Lys Leu Leu Gly Asn Leu Phe Ile Ser Gly Glu Ser Gln
        35                  40                  45

cag aac tta aat aac aag att att cta gaa aag gat acc gta act ttc     192
Gln Asn Leu Asn Asn Lys Ile Ile Leu Glu Lys Asp Thr Val Thr Phe
    50                  55                  60

cag gaa att gac ttt aaa atc aga aaa tac ctt atg gat aat tat aaa     240
Gln Glu Ile Asp Phe Lys Ile Arg Lys Tyr Leu Met Asp Asn Tyr Lys
65                  70                  75                  80

att tat gac gct act tct cct tat gta agc ggc aga atc gaa att ggc     288
Ile Tyr Asp Ala Thr Ser Pro Tyr Val Ser Gly Arg Ile Glu Ile Gly
                85                  90                  95

aca aaa gat gga aaa cat gag caa ata gac tta ttt gac tca cca aat     336
Thr Lys Asp Gly Lys His Glu Gln Ile Asp Leu Phe Asp Ser Pro Asn
```

```
                   100                    105                     110

gaa ggg act aga tca gat att ttt gca aaa tat aaa gat aat aga att    384
Glu Gly Thr Arg Ser Asp Ile Phe Ala Lys Tyr Lys Asp Asn Arg Ile
            115                 120                 125

atc aat atg aag aac ttt agt cat ttc gat att tat ctt gaa aaa       429
Ile Asn Met Lys Asn Phe Ser His Phe Asp Ile Tyr Leu Glu Lys
        130                 135                 140

taa                                                                432
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<210> 6
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 6
Asp Ser Lys Lys Asp Ile Ser Asn Val Lys Ser Asp Leu Leu Cys Ala
 1               5                  10                  15
Tyr Thr Ile Thr Pro Ile Glu Gly Arg Thr Pro Ala Gln Asn Asn Lys
            20                  25                  30
Val Asn His Lys Leu Leu Gly Asn Leu Phe Ile Ser Gly Glu Ser Gln
        35                  40                  45
Gln Asn Leu Asn Asn Lys Ile Ile Leu Glu Lys Asp Thr Val Thr Phe
    50                  55                  60
Gln Glu Ile Asp Phe Lys Ile Arg Lys Tyr Leu Met Asp Asn Tyr Lys
65                  70                  75                  80
Ile Tyr Asp Ala Thr Ser Pro Tyr Val Ser Gly Arg Ile Glu Ile Gly
                85                  90                  95
Thr Lys Asp Gly Lys His Glu Gln Ile Asp Leu Phe Asp Ser Pro Asn
            100                 105                 110
Glu Gly Thr Arg Ser Asp Ile Phe Ala Lys Tyr Lys Asp Asn Arg Ile
            115                 120                 125
Ile Asn Met Lys Asn Phe Ser His Phe Asp Ile Tyr Leu Glu Lys
        130                 135                 140
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<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
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<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence
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```
<220>
<223> Primer

<400> 8
ctgaattctt atttttcaag at                                    22

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
gatttacttt gtgcatacac                                       20

<210> 10
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
atattctttg ttctcaca                                         18

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 11
gatttacttt gtgcatacac                                       20

<210> 12
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
gaagggactc aatcagatat ttttgc                                26

<210> 13
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer
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```
<400> 13
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<210> 14
<211> 22
<212> DNA
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<220>
<223> Primer

<400> 14
gattataaag attccagggt aa                                             22

<210> 15
<211> 20
<212> DNA
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<220>
<223> Primer

<400> 15
gtgtatgcac aaagtaaatc                                                20

<210> 16
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
tataagaaac aagagtgt                                                  18

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
gtgtatgcac aaagtaaatc                                                20

<210> 18
<211> 26
<212> DNA
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<220>
<223> Primer

<400> 18
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gacaaaatat ctgattgagt cccttc   26

<210> 19
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
acgaccttcg ataggagtta tagtgtat   28

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
ttaccctgga atctttataa tc   22

<210> 21
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 21
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 1   5   10

<210> 22
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 22
Arg Ala Asp Leu Ile Ala Tyr Leu Lys Gln Ala Thr Lys
 1   5   10